

FIG. 1

ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala	48
1 5 10 15	
TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn	96
20 25 30	
GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln	144
35 40 45	
TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser	192
50 55 60	
GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC Ala Glu Gly Trp Gly Pro Glu Pro Leu Pro Tyr Ser Arg Ala Phe	240
65 70 75 80	
GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr	288
85 90 95	
TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg	336
100 105 110	
TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His	384
115 120 125	
GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly	432
130 135 140	
GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys	480
145 150 155 160	
GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro	528
165 170 175	
AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg	576
180 185 190	
CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln	624
195 200 205	
CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu	672
210 215 220	

FIG. 2

AMINO ACID ALIGNMENT BETWEEN CRIPTO AND CRIPTIN

10	20	30	40
1 M T W R H H V R L L F T V S L A L Q I I N L G N S Y Q R E K H N G G R G E V T K HGS Cryptin			
1 W - - H A A I S K V F E L G L - - V A G L G - - H Q E F A R P S R G Y L A - Human Cripto			
<hr/>			
50	60	70	80
41 V A T Q K H R Q S P L N W T S S H F G E V T G S A E G W G P E E P L P Y S R A F HGS Cryptin			
32 - - - - F R D D S I - W P Q E E - P A I R P R S S Q R V P P M G I Q H S K E L Human Cripto			
<hr/>			
90	100	110	120
81 G E R G A S A R P R C C R N G G T C V I L G S F C V C D A H F T G R Y C E H D Q R R HGS Cryptin			
65 N R T - - - - C C L N G G T C M L G S F C A C P P S P Y G R N C E H D V R K Human Cripto			
<hr/>			
130	140	150	160
121 S E C G A L E H G A W T L R A C H L C R C I F G A H H C L P L Q T P D R C D P - HGS Cryptin			
99 E N C G S V P H D T W L P K K C S L C K C W H G Q D R C F P Q A F L P G C D G L Human Cripto			
<hr/>			
170	< 180	190	200
160 - - K D F L A S H A H G - P S A G G A P S L L L L P C A L L H R L L R P D A HGS Cryptin			
139 V M D E H L V A S R T P E L E P S A R T T T F L M V G I C L S I Q S Y Y Human Cripto			
<hr/>			
210	220		
196 P A H P R S L V P S V L Q R E R R P C G R P G L G H R L			
174			
HGS Cryptin Human Cripto			

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.